e) detecting one or more nucleotide sequence differences in the members of said collection of step (d) with a method that detects one or more nucleotide differences with respect to a reference sequence,

wherein said steps (b) and (c) follow step (a) but can occur in either order, followed thereafter by steps (d) and (e) in that order, wherein said steps (a)-(e) enrich for and identify a nucleic acid sequence difference with respect to a reference sequence.

69. (Twice amended) A method of enriching for and identifying nucleic acid sequence differences with respect to a reference sequence comprising:

a) fragmenting a genomic nucleic acid sample from one or more individuals;

b) physically separating a subset of said nucleic acid fragments based on the size of the fragments;

c) detecting one or more nucleic acid sequence differences with respect to a reference sequence in the members of said separated molecules of step (b), wherein steps (a)-(c) enrich for and identify a nucleic acid sequence difference with respect to a reference sequence.

159. (New) The method of claim 1 wherein said subset of nucleic acid molecules having a sequence that binds to said sequence-specific binding activity comprises less than every molecule in the population of nucleic acid molecules in said sample.

REMARKS

At the outset, Applicants wish to thank Examiner Chakrabarti for the telephone interview of February 12, 2002, in which distinctions of the claimed invention over the Oefner et al. reference, alone and in combination with the Bloch et al. and Fox et al. references, were pointed out.

Claims 1-3, 57-74 and 145-158 are pending. Applicants note that there is a discrepancy between the pending claims acknowledged in the Final Office Action and the pending claims filed. Specifically, the Final Office Action lists claims 1-3, 57-74 and 145-156 as pending, while new claims 157 and 158, submitted in response to the non-final Office Action mailed February 28, 2001, were not entered. New claims 157 and